

% SEQUENCE SIMILARITY TO HUMAN OP-1 SEVEN-CYSTEINE DOMAIN

APPROVED	O.G. FIG.
BY	CLASS/SUBCLASS
DRAFTSMAN	

006221*07718560

SEQUENCE	% SIMILARITY	% NON CONSERVATIVE
hOP-1	100	0
mOP-1	100	0
hOP-2	97	3
mOP-2	97	3
BMP-5	97	3
BMP-6	96	4
Vgr-1(PT)	94	6
OP-3	91	9
60A	90	10
BMP-4	90	10
BMP-2	89	11
dpp	87	13
UNIVIN	87	13
dpp(PT)	86	14
Vg-1	86	14
CDMP-1	85	15
CDMP-3	83	17
GDF-3	83	17
CDMP-2	82	18
DORSALIN	79	21
GDF-1(PT)	78	22
GDF-10	78	22
BMP-3b	78	22
BMP-10	78	23
BMP-3	78	23
SCREW	77	23
ADMP	77	24
TGF- β 2	73	27
GDF-1	73	28
BMP-9	73	28
NODAL	71	29
Inhibin β A	71	29
BMP-15	71	29
TGF- β 3	69	31
Inhibin β B	69	31
Inhibin β C	69	31
TGF- β 5	67	33
TGF- β 1	67	33
GDF-12	67	33
GDF-11	66	34
TGF- β 4	66	34
GDF-9	66	34
GDF-8	64	36
BMP-11	60	40
GDNF	49	51

FIG. 1

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APPROVED	O.G. FIG.
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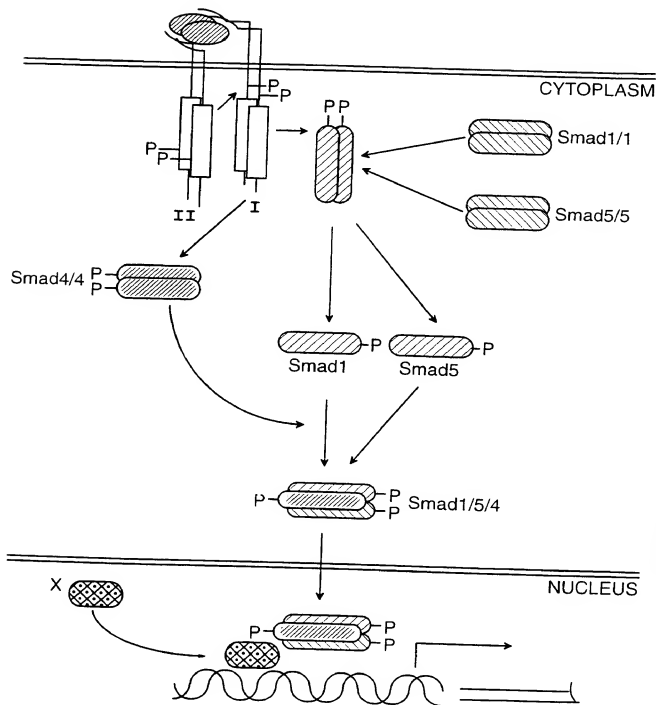
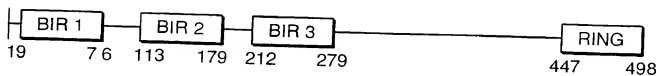


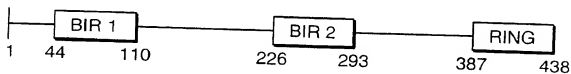
FIG. 2

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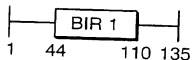
DIAP FULL LENGTH (498 A.A)



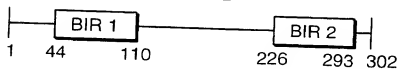
DIAP FULL LENGTH (438 A.A)



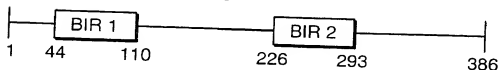
TRUNCATED FORM 1 (TF-1)



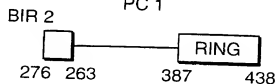
TF 2



TF 3



PC 1



TF 4



FIG. 3

APPROVED	O.G. FIG.
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APPROVED	O.G. FIG.
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	PC1	DIAP1	DIAP2
TKV wt	+++	++	-
TKV QD	++	++	-
TKV KR	+	+	-
TKV Δ JM	-	-	ND
SAX	-	-	-
PUNT	-	-	-

ND : NOT DONE

FIG. 4

	DIAP1	TF 1	TF 2	TF 3	PC1	TF 4
TKV wt	++	-	-	-	+++	++
SAX	-	ND	ND	ND	-	-
PUNT	-	ND	ND	ND	-	-

ND : NOT DONE

FIG. 5

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APPROVED	0.G. FIG.
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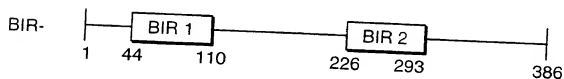
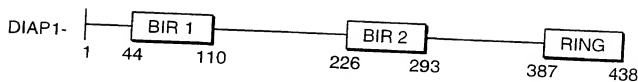


FIG. 6